

RAW SEQUENCE LISTING

EFS

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/553,906 D
Source: IFW
Date Processed by STIC: 1/5/07

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 01/05/2007

PATENT APPLICATION: US/10/553,906D

TIME: 14:14:14

Input Set : N:\efs\01_05_07\10553906_efs\ALBI-41348-sequence_ST25.txt

Output Set: N:\CRF4\01052007\J553906D.raw

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3 <110> APPLICANT: Bergman, Tomas
4      Duan, Rui-Dong
5      Nilsson, Ake
7 <120> TITLE OF INVENTION: Human Alkaline Sphingomyelinase and Use Thereof
9 <130> FILE REFERENCE: ALBI 41348
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/553,906D
C--> 12 <141> CURRENT FILING DATE: 2005-10-21
14 <150> PRIOR APPLICATION NUMBER: US 60/320,139
15 <151> PRIOR FILING DATE: 2003-04-24
17 <150> PRIOR APPLICATION NUMBER: US 60/481,598
18 <151> PRIOR FILING DATE: 2003-11-05
20 <160> NUMBER OF SEQ ID NOS: 18
22 <170> SOFTWARE: PatentIn version 3.4
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 458
26 <212> TYPE: PRT
27 <213> ORGANISM: Homo sapiens
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36          20          25          30
39 Leu Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asn Tyr Asp Gln Asp
40          35          40          45
43 Val Asp Thr Pro Asn Leu Asp Ala Met Ala Arg Asp Gly Val Lys Ala
44          50          55          60
47 Arg Tyr Met Thr Pro Ala Phe Val Thr Met Thr Ser Pro Cys His Phe
48 65          70          75          80
51 Thr Leu Val Thr Gly Lys Tyr Ile Glu Asn His Gly Val Val His Asn
52          85          90          95
55 Met Tyr Tyr Asn Thr Thr Ser Lys Val Lys Leu Pro Tyr His Ala Thr
56          100         105         110
59 Leu Gly Ile Gln Arg Trp Trp Asp Asn Gly Ser Val Pro Ile Trp Ile
60          115         120         125
63 Thr Ala Gln Arg Gln Gly Leu Arg Ala Gly Ser Phe Phe Tyr Pro Gly
64          130         135         140
67 Gly Asn Val Thr Tyr Gln Gly Val Ala Val Thr Arg Ser Arg Lys Glu
68 145         150         155         160
71 Gly Ile Ala His Asn Tyr Lys Asn Glu Thr Glu Trp Arg Ala Asn Ile
72          165         170         175
75 Asp Thr Val Met Ala Trp Phe Thr Glu Glu Asp Leu Asp Leu Val Thr
76          180         185         190
79 Leu Tyr Phe Gly Glu Pro Asp Ser Thr Gly His Arg Tyr Gly Pro Glu

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83	Ser Pro Glu Arg Arg Glu Met Val Arg Gln Val Asp Arg Thr Val Gly		
84	210	215	220
87	Tyr Leu Arg Glu Ser Ile Ala Arg Asn His Leu Thr Asp Arg Leu Asn		
88	225	230	235
91	Leu Ile Ile Thr Ser Asp His Gly Met Thr Thr Val Asp Lys Arg Ala		
92	245	250	255
95	Gly Asp Leu Val Glu Phe His Lys Phe Pro Asn Phe Thr Phe Arg Asp		
96	260	265	270
99	Ile Glu Phe Glu Leu Leu Asp Tyr Gly Pro Asn Gly Met Leu Leu Pro		
100	275	280	285
103	Lys Glu Gly Arg Leu Glu Lys Val Tyr Asp Ala Leu Lys Asp Ala His		
104	290	295	300
107	Pro Lys Leu His Val Tyr Lys Lys Glu Ala Phe Pro Glu Ala Phe His		
108	305	310	315
111	Tyr Ala Asn Asn Pro Arg Val Thr Pro Leu Leu Met Tyr Ser Asp Leu		
112	325	330	335
115	Gly Tyr Val Ile His Gly Arg Ile Asn Val Gln Phe Asn Asn Gly Glu		
116	340	345	350
119	His Gly Phe Asp Asn Lys Asp Met Asp Met Lys Thr Ile Phe Arg Ala		
120	355	360	365
123	Val Gly Pro Ser Phe Arg Ala Gly Leu Glu Val Glu Pro Phe Glu Ser		
124	370	375	380
127	Val His Val Tyr Glu Leu Met Cys Arg Leu Leu Gly Ile Val Pro Glu		
128	385	390	395
131	Ala Asn Asp Gly His Leu Ala Thr Leu Leu Pro Met Leu His Thr Glu		
132	405	410	415
135	Ser Ala Leu Pro Pro Asp Ala Leu Leu Val Ala Asp Gly Pro Cys Leu		
136	420	425	430
139	Pro Ser Leu Ser Gln Ala Lys Gly Cys Met Pro Leu Ser Pro Ala Ala		
140	435	440	445
143	Pro Thr Pro Ala Trp Leu Leu Trp Cys Trp		
144	450	455	
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148	<211> LENGTH: 1701		
149	<212> TYPE: DNA		
150	<213> ORGANISM: Homo sapiens		
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155	cgctcctggc tcccggggcc ggagcaccgg tacaaagtca gggctcccag aacaagctgc	120	
157	tcctggtgtc cttcgacggc ttccgctgga actacgacca ggacgtggac accccaacc	180	
159	tggacgccat ggcccagagc ggggtgaagg cacgctacat gacccccgcc tttgtcacca	240	
161	tgaccagccc ctgccacttc accctgggtca ccggcaaata tatcgagaac cacgggggtgg	300	
163	ttcacaacat gtactacaac accaccagca aggtgaagct gccctaccac gccacgctgg	360	
165	gcatccagag gtggtgggac aacggcagcg tgcccatctg gatcacagcc cagaggcagg	420	
167	gcctgagggc tggctccttc ttctaccggt gcgggaacgt cacctaccaa ggggtggctg	480	
169	tgacgcggag ccggaagaa ggcacgcac acaactacaa aaatgagacg gagtggagag	540	
171	cgaacatcga cacagtgatg gcgtgggttc cagaggagga cctggatctg gtcacactct	600	
173	acttcgggga gccggactcc acgggccaca ggtacggccc cgagtccccg gagaggaggg	660	

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175 agatggtgcg gcaggtggac cggaccgtgg gctacctccg ggagagcatc gcgcgcaacc 720
177 acctcacaga ccgcctcaac ctgatcatca catccgacca cggcatgacg accgtggaca 780
179 aacgggctgg cgacctggtt gaattccaca agttcccca cttcaccttc cgggacatcg 840
181 agtttgagct cctggactac ggaccaaacg ggatgctgct ccctaaagaa gggaggctgg 900
183 agaaggtgta cgatgccctc aaggacgccc accccaagct ccacgtctac aagaaggagg 960
185 cgttccccga ggccttccac tacgccaaca accccagggt cacaccctg ctgatgtaca 1020
187 gcgaccttgg ctacgtcatc catgggagaa ttaacgtcca gttcaacaat ggggagcacg 1080
189 gctttgacaa caaggacatg gacatgaaga ccatcttccg cgctgtgggc cctagcttca 1140
191 gggcgggcct ggaggtggag ccctttgaga gcgtccacgt gtacgagctc atgtgccggc 1200
193 tgctgggcat cgtgcccagag gccaacgatg ggcacctagc tactctgctg cccatgctgc 1260
195 acacagaatc tgctcttccg cctgatgctc tgctggtcgc ggacggaccc tgcctcccca 1320
197 gcttatccca ggccagaggc tgcatgccac tgtccccggc agcgccaacc cctgcttggc 1380
199 tgttatggtg ctggtaataa gcctgcagcc caggtcctaaa gcccccggcg agccggtccc 1440
201 ataaccggcc ccctgcccct gccctgctc ctgctcctcc ccttcgggcc ccctcctcct 1500
203 gcaaaacccg ctcccgaagc ggcgctgccg tctgcagcca cgcggggggc cgcgggagtc 1560
205 ttctgcgggc gctggaacct gcagaccgag cctcggtcag ctgggagggg cccgccccgg 1620
207 cacaagcac ccatgggaat aaaggccaag ccgcgacagt cagcaaaaaa aaaaaaaaaa 1680
209 aaaaaaaaaa aaaaaaaaaa a 1701

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212 <210> SEQ ID NO: 3

213 <211> LENGTH: 18

214 <212> TYPE: PRT

215 <213> ORGANISM: Homo sapiens

217 <400> SEQUENCE: 3

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220 1 5 10 15

223 Lys Tyr

227 <210> SEQ ID NO: 4

228 <211> LENGTH: 458

229 <212> TYPE: PRT

230 <213> ORGANISM: Homo sapiens

232 <400> SEQUENCE: 4

234 Met Arg Gly Pro Ala Val Leu Leu Thr Val Ala Leu Ala Thr Leu Leu

235 1 5 10 15

238 Ala Pro Gly Ala Gly Ala Pro Val Gln Ser Gln Gly Ser Gln Asn Lys

239 20 25 30

242 Leu Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asn Tyr Asp Gln Asp

243 35 40 45

246 Val Asp Thr Pro Asn Leu Asp Ala Met Ala Arg Asp Gly Val Lys Ala

247 50 55 60

250 Arg Tyr Met Thr Pro Ala Phe Val Thr Met Thr Ser Pro Cys His Phe

251 65 70 75 80

254 Thr Leu Val Thr Gly Lys Tyr Ile Glu Asn His Gly Val Val His Asn

255 85 90 95

258 Met Tyr Tyr Asn Thr Thr Ser Lys Val Lys Leu Pro Tyr His Ala Thr

259 100 105 110

262 Leu Gly Ile Gln Arg Trp Trp Asp Asn Gly Ser Val Pro Ile Trp Ile

263 115 120 125

266 Thr Ala Gln Arg Gln Gly Leu Arg Ala Gly Ser Phe Phe Tyr Pro Gly

267 130 135 140

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270 Gly Asn Val Thr Tyr Gln Gly Val Ala Val Thr Arg Ser Arg Lys Glu
271 145                               150                               155                               160
274 Gly Ile Ala His Asn Tyr Lys Asn Glu Thr Glu Trp Arg Ala Asn Ile
275                               165                               170                               175
278 Asp Thr Val Met Ala Trp Phe Thr Glu Glu Asp Leu Asp Leu Val Thr
279                               180                               185                               190
282 Leu Tyr Phe Gly Glu Pro Asp Ser Thr Gly His Arg Tyr Gly Pro Glu
283                               195                               200                               205
286 Ser Pro Glu Arg Arg Glu Met Val Arg Gln Val Asp Arg Thr Val Gly
287                               210                               215                               220
290 Tyr Leu Arg Glu Ser Ile Ala Arg Asn His Leu Thr Asp Arg Leu Asn
291 225                               230                               235                               240
294 Leu Ile Ile Thr Ser Asp His Gly Met Thr Thr Val Asp Lys Arg Ala
295                               245                               250                               255
298 Gly Asp Leu Val Glu Phe His Lys Phe Pro Asn Phe Thr Phe Arg Asp
299                               260                               265                               270
302 Ile Glu Phe Glu Leu Leu Asp Tyr Gly Pro Asn Gly Met Leu Leu Pro
303                               275                               280                               285
306 Lys Glu Gly Arg Leu Glu Lys Val Tyr Asp Ala Leu Lys Asp Ala His
307                               290                               295                               300
310 Pro Lys Leu His Val Tyr Lys Lys Glu Ala Phe Pro Glu Ala Phe His
311 305                               310                               315                               320
314 Tyr Ala Asn Asn Pro Arg Val Thr Pro Leu Leu Met Tyr Ser Asp Leu
315                               325                               330                               335
318 Gly Tyr Val Ile His Gly Arg Ile Asn Val Gln Phe Asn Asn Gly Glu
319                               340                               345                               350
322 His Gly Phe Asp Asn Lys Asp Met Asp Met Lys Thr Ile Phe Arg Ala
323                               355                               360                               365
326 Val Gly Pro Ser Phe Arg Ala Gly Leu Glu Val Glu Pro Phe Glu Ser
327                               370                               375                               380
330 Val His Val Tyr Glu Leu Met Cys Arg Leu Leu Gly Ile Val Pro Glu
331 385                               390                               395                               400
334 Ala Asn Asp Gly His Leu Ala Thr Leu Leu Pro Met Leu His Thr Glu
335                               405                               410                               415
338 Ser Ala Leu Pro Pro Asp Gly Arg Pro Thr Leu Leu Pro Lys Gly Arg
339                               420                               425                               430
342 Ser Ala Leu Pro Pro Ser Ser Arg Pro Leu Leu Val Met Gly Leu Leu
343                               435                               440                               445
346 Gly Thr Val Ile Leu Leu Ser Glu Val Ala
347                               450                               455

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350 <210> SEQ ID NO: 5
351 <211> LENGTH: 1878
352 <212> TYPE: DNA
353 <213> ORGANISM: Homo sapiens
356 <220> FEATURE:
357 <221> NAME/KEY: misc_feature
358 <222> LOCATION: (905)..(905)
359 <223> OTHER INFORMATION: n is a, c, g, or t
361 <400> SEQUENCE: 5

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362 gtccatctgg aaggcccagc atgagaggcc cggccgtcct cctcactgtg gctctggcca      60
364 cgctcctggc tcccggggcc ggagcaccgg tacaaagtca gggctcccag aacaagctgc      120
366 tcctggtgtc cttcgacggc ttccgctgga actacgacca ggacgtggac accccaacc      180
368 tggacgccat ggcccagagc ggggtgaagg cacgctacat gacccccgcc tttgtcacca      240
370 tgaccagccc ctgccacttc accctggtca ccggcaaata tatcgagaac cacggggtgg      300
372 ttcacaacat gtactacaac accaccagca aggtgaagct gccctaccac gccacgctgg      360
374 gcatccagag gtggtgggac aacggcagcg tgcccatctg gatcacagcc cagaggcagg      420
376 gcctgagggc tggctccttc ttctacccgg gcgggaacgt cacctaccaa ggggtggctg      480
378 tgacgcggag ccggaagaa ggcattcgac acaactacaa aaatgagacg gagtggagag      540
380 cgaacatcga cacagtgatg gcgtggttca cagaggagga cctggatctg gtcacactct      600
382 acttcgggga gccggactcc acgggccaca ggtacggccc cgagtccccg gagaggagg      660
384 agatggtgcg gcaggtggac cggaccgtgg gctacctccg ggagagcatc gcgcgcaacc      720
386 acctcacaga ccgcctcaac ctgatcatca catccgacca cggcatgacg accgtggaca      780
388 aacgggctgg cgacctggtt gaattccaca agttcccca cttcaccttc cgggacatcg      840
390 agtttgagct cctggactac ggaccaaacy ggatgctgct ccctaaagaa gggaggctgg      900
W--> 392 agaangtgta cgatgccctc aaggacgccc accccaagct ccacgtctac aagaaggagg      960
394 cgttccccga ggccttccac tacgccaaca accccagggt cacaccctg ctgatgtaca     1020
396 gcgaccttgg ctacgtcatc catgggagaa ttaacgtcca gttcaacaat ggggagcacg     1080
398 gctttgacaa caaggacatg gacatgaaga ccatcttcgg cgctgtgggc cctagcttca     1140
400 gggcgggcct ggaggtggag ccctttgaga gcgtccacgt gtacgagctc atgtgccggc     1200
402 tgctgggcat cgtgcccag gccaacgatg ggcacctagc tactctgctg cccatgctgc     1260
404 acacagaatc tgctcttcgg cctgatggaa ggcctactct cctgcccagg ggaagatctg     1320
406 ctctcccgcc cagcagcagg cccctcctcg tgatgggact gctggggacc gtgattcttc     1380
408 tgtctgaggt cgcataacgc cccatggctc aaggaagccg ccgggagctg cccgcaggcc     1440
410 ctgggcccgc tgtctcgctg cgatgctctg ctggtcgcg acggacctg cctccccagc     1500
412 ttatcccagg ccagaggctg catgccactg tccccggcag cgccaacccc tgcttggtg      1560
414 ttatggtgct ggtaataagc ctgcagccc aggtccagag cccccggcga gccggtccca      1620
416 taaccggccc cctgcccctg cccctgctcc tgctcctccc cttcggggccc cctcctcctg      1680
418 caaaacccgc tcccgaagcg gcgctgccgt ctgcagccac gcggggggcg gcgggagctc      1740
420 tgcggggcgt ggaacctgca gaccggcct cggtcagctg ggagggggccc gcccggcac      1800
422 aaagcaccca tgggaataaa ggccaagccg cgacagtcag caaaaaaaaa aaaaaaaaaa      1860
424 aaaaaaaaaa aaaaaaaaaa                                     1878
427 <210> SEQ ID NO: 6
428 <211> LENGTH: 415
429 <212> TYPE: PRT
430 <213> ORGANISM: Homo sapiens
432 <400> SEQUENCE: 6
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438 Ala Pro Gly Ala Gly Ala Pro Val Gln Ser Gln Gly Ser Gln Asn Lys
439          20          25          30
442 Leu Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asn Tyr Asp Gln Asp
443          35          40          45
446 Val Asp Thr Pro Asn Leu Asp Ala Met Ala Arg Asp Gly Val Lys Ala
447          50          55          60
450 Arg Tyr Met Thr Pro Ala Phe Val Thr Met Thr Ser Pro Cys His Phe
451 65          70          75          80
454 Thr Leu Val Thr Gly Lys Tyr Ile Glu Asn His Gly Val Val His Asn
455          85          90          95

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 905

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:10,11,12,13,14,15,17,18

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:900